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OM protein - protein search, using sw model

Run on: December 20, 2004, 13:36:46 ; Search time 153 Seconds
(without alignments)
35.170 Million cell updates/sec

Title: US-10-006-593-2

Perfect score: 80
Sequence: 1 IEGLPTLRQWLARAP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	15	ABP51670	ABP51670 Thrombopo
2	80	100.0	15	ADQ16585	Adq16585 TPO mimet
3	80	100.0	18	ABP51687	ABP51687 TPO mimet
4	80	100.0	18	ABP51689	ABP51689 TPO mimet
5	80	100.0	18	ABP51688	ABP51688 TPO mimet
6	80	100.0	18	ABP51686	ABP51686 TPO mimet
7	80	100.0	18	ABP51693	ABP51693 TPO mimet
8	80	100.0	18	ABP51684	ABP51684 TPO mimet
9	80	100.0	18	ABP51691	ABP51691 TPO mimet
10	80	100.0	18	ABP51690	ABP51690 TPO mimet
11	80	100.0	18	ABP51675	ABP51675 TPO mimet
12	80	100.0	18	ADQ16611	Adq16611 TPO mimet
13	80	100.0	18	ADQ16619	Adq16619 TPO mimet
14	80	100.0	18	ADQ16621	Adq16621 TPO mimet
15	80	100.0	18	ADQ16646	Adq16646 TPO mimet
16	80	100.0	18	ADQ16615	Adq16615 TPO mimet
17	80	100.0	18	ADQ16625	Adq16625 TPO mimet
18	80	100.0	18	ADQ16617	Adq16617 TPO mimet
19	80	100.0	18	ADQ16629	Adq16629 TPO mimet
20	80	100.0	18	ADQ16623	Adq16623 TPO mimet
21	80	100.0	22	ADQ16710	Adq16710 Immunoglo
22	80	100.0	128	ADQ16705	Adq16705 Modified
23	80	100.0	225	ADQ16704	Adq16704 Modified
24	80	100.0	472	ABP51695	ABP51695 SGI.1-TPO
25	80	100.0	472	ADQ16647	Adq16647 Immunoglo

26	73	91.2	14	2	AAW09463	AAW09463 Thrombopo
27	73	91.2	14	2	AAW09468	AAW09468 Thrombopo
28	73	91.2	14	2	AAW33030	AAW33030 Thrombopo
29	73	91.2	14	2	AAW33034	AAW33034 Thrombopo
30	73	91.2	14	2	AAW36774	AAW36774 Thrombopo
31	73	91.2	14	2	AD124843	AD124843 AP 12505
32	73	91.2	14	3	AAV96515	AAV96515 Thrombopo
33	73	91.2	14	3	AAV96515	AAV96515 TPO-mimet
34	73	91.2	14	4	AAU25827	AAU25827 Human thr
35	73	91.2	14	4	AAU26004	AAU26004 Human thr
36	73	91.2	14	5	ABR72853	ABR72853 TPO mimet
37	73	91.2	14	5	ABP51669	ABP51669 Thrombopo
38	73	91.2	14	5	AAE18011	AAE18011 Human 11g
39	73	91.2	14	6	ABG71747	ABG71747 TPO recep
40	73	91.2	14	7	ABR62907	ABR62907 Thrombopo
41	73	91.2	14	7	ADC33697	ADC33697 Erythro
42	73	91.2	14	7	ADN59652	ADN59652 Thrombopo
43	73	91.2	14	8	ADL27293	ADL27293 Amino aci
44	73	91.2	14	8	ADM72483	ADM72483 TPO mimet
45	73	91.2	14	8	ADQ16584	Adq16584 Agonist T

ALIGNMENTS

RESULT 1
ABP51670
ID ABP51670 standard; peptide; 15 AA.
XX
AC ABP51670;
XX
DT 01-OCT-2002 (first entry)
XX
DE Thrombopoietin (TPO) agonist mimetic peptide SEQ ID NO:2.
XX
KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW complementarity determining region; immunoglobulin; antiaenaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200246238-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US047656.
XX
PR 05-DEC-2000; 2000US-0251448P.
PR 04-MAY-2001; 2001US-0288889P.
PR 29-MAY-2001; 2001US-0294068P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Barbae-Frederickson S, Renshaw M;
XX WPI; 2002-566610/60.
XX
PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.
XX
PS Claim 19; Page 6; 113pp; English.
XX
CC The present invention describes an immunoglobulin molecule or its fragment
CC (i) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (i) has
CC antiaenaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of

CC the exemplification of the present invention
XX
SQ Sequence 18 AA:

Query Match 100.0%; Score 80; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAAP 15
| | | | | | | | | | | | | | | | | |
Db 3 IEGPTLRQWLAAAP 17

RESULT 4

ABP51689
ID ABP51689 standard; peptide; 18 AA.

XX ABP51689;

XX 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:41.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KM complementarity determining region; immunoglobulin; antinaemic;
KM haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbae-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73367.

PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
CC (1) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (1) has
CC antinaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (1) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (1) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (1) is contacted with haematopoietic
CC stem cells or their progenitors. (1) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,

CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 18 AA:

Query Match 100.0%; Score 80; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAAP 15
| | | | | | | | | | | | | | | | | |
Db 3 IEGPTLRQWLAAAP 17

RESULT 5

ABP51688
ID ABP51688 standard; peptide; 18 AA.

XX ABP51688;

XX 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:39.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KM complementarity determining region; immunoglobulin; antinaemic;
KM haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbae-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73366.

PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
CC (1) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (1) has
CC antinaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (1) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (1) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (1) is contacted with haematopoietic
CC stem cells or their progenitors. (1) is useful for diagnostics or

CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of hematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 CC
 SQ Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGLPTLROWLAAAP 15
 |||||
 3 IEGLPTLROWLAAAP 17

RESULT 6
 ABP51686
 ID ABP51686 standard; peptide; 18 AA.
 XX
 AC ABP51686;
 XX
 DT 01-OCT-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:35.
 XX
 DE TPO mimetic peptide SEQ ID NO:35.
 XX
 KM TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KM complementarity determining region; immunoglobulin; antianemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200246238-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US047656.
 XX
 PR 05-DEC-2000; 2000US-0251448P.
 PR 04-MAY-2001; 2001US-0288889P.
 PR 29-MAY-2001; 2001US-0294068P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Barbas-Frederickson S, Renshaw M;
 PI WPI; 2002-566610/60.
 DR N-PSDB; ABQ73364.
 XX

PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.
 XX
 XX Claim 20; Fig 5; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
 CC (1) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has
 CC antianemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the

CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of hematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 CC
 SQ Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGLPTLROWLAAAP 15
 |||||
 3 IEGLPTLROWLAAAP 17

RESULT 7
 ABP51693
 ID ABP51693 standard; peptide; 18 AA.
 XX
 AC ABP51693;
 XX
 DT 01-OCT-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:49.
 XX
 DE TPO mimetic peptide SEQ ID NO:49.
 XX
 KM TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KM complementarity determining region; immunoglobulin; antianemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200246238-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US047656.
 XX
 PR 05-DEC-2000; 2000US-0251448P.
 PR 04-MAY-2001; 2001US-0288889P.
 PR 29-MAY-2001; 2001US-0294068P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Barbas-Frederickson S, Renshaw M;
 PI WPI; 2002-566610/60.
 DR N-PSDB; ABQ73371.
 XX

PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.
 XX
 XX Claim 20; Fig 5; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
 CC (1) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has
 CC antianemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC production. (1) with a region where amino acid residues corresponding to

CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (I) is contacted with haematopoietic
CC stem cells or their progenitors. (I) is useful for diagnostics or
CC therapeutic, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51696 represent sequences used in
CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 2,1e-06; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

OY 1 IEGPTLRQWLARAP 15

DB 3 IEGPTLRQWLARAP 17

RESULT 8

ABP51684 ID ABP51684 standard; peptide; 18 AA.

XX ABP51684;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:31.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KM complementarity determining region; immunoglobulin; antianaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

XX WO200246238-A2.

PN 13-JUN-2002.

PD 05-DEC-2001; 2001WO-US047656.

XX 05-DEC-2001; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Fredrickson S, Renshaw M;

XX WPI; 2002-566610/60.

DR N-PSDB; ABQ73362.

XX A novel immunogen molecule comprising a region in which amino acid

PT residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

PT thrombopoietin mimetic.

XX Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
CC (I) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (I) has
CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (I) is contacted with

CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (I) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (I) is contacted with haematopoietic
CC stem cells or their progenitors. (I) is useful for diagnostics or
CC therapeutic, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51696 represent sequences used in
CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 2,1e-06; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

OY 1 IEGPTLRQWLARAP 15

DB 3 IEGPTLRQWLARAP 17

RESULT 9

ABP51691 ID ABP51691 standard; peptide; 18 AA.

XX ABP51691;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:45.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KM complementarity determining region; immunoglobulin; antianaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

XX WO200246238-A2.

PN 13-JUN-2002.

PD 05-DEC-2001; 2001WO-US047656.

XX 05-DEC-2001; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Fredrickson S, Renshaw M;

XX WPI; 2002-566610/60.

DR N-PSDB; ABQ73369.

XX A novel immunogen molecule comprising a region in which amino acid

PT residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

PT thrombopoietin mimetic.

XX Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
CC (I) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (I) has
CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful

CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-QY 1 IEGPTLRQWLARAP 15
 |||||
 Db 3 IEGPTLRQWLARAP 17

RESULT 10

ABP51690
 ID ABP51690 standard; peptide; 18 AA.

XX
 AC ABP51690;

XX
 DT 01-OCT-2002 (first entry)

XX
 DE TPO mimetic peptide SEQ ID NO:43.

XX
 KM TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KM haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX
 OS Homo sapiens.

XX
 OS Synthetic.

XX
 PN WO200246238-A2.

XX
 PD 13-JUN-2002.

XX
 PF 05-DEC-2001; 2001WO-US047656.

XX
 PR 05-DEC-2000; 2000US-0251448P.

XX
 PR 04-MAY-2001; 2001US-0288889P.

XX
 PR 29-MAY-2001; 2001US-0294068P.

XX
 PA (ALEX-) ALEXION PHARM INC.

XX
 PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX
 DR WPI, 2002-566610/60.

XX
 DR N-PSDB; ABQ73368.

XX
 PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

XX
 PS Claim 20; Fig 5; 113pp; English.

XX
 CC The present invention describes an immunoglobulin molecule or its fragment
 CC (1) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as

CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARAP 15
 |||||
 Db 3 IEGPTLRQWLARAP 17

RESULT 11

ABP51675
 ID ABP51675 standard; peptide; 18 AA.

XX
 AC ABP51675;

XX
 DT 01-OCT-2002 (first entry)

XX
 DE TPO mimetic antibody related peptide graft SEQ ID NO:66.

XX
 KM TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KM haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX
 OS Homo sapiens.

XX
 OS Synthetic.

XX
 PN WO200246238-A2.

XX
 PD 13-JUN-2002.

XX
 PF 05-DEC-2001; 2001WO-US047656.

XX
 PR 05-DEC-2000; 2000US-0251448P.

XX
 PR 04-MAY-2001; 2001US-0288889P.

XX
 PR 29-MAY-2001; 2001US-0294068P.

XX
 PA (ALEX-) ALEXION PHARM INC.

XX
 PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX
 DR WPI, 2002-566610/60.

XX
 PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

XX
 PS Example 4; Page 55; 113pp; English.

XX
 CC The present invention describes an immunoglobulin molecule or its fragment
 CC (1) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has

CC antihaemic, haemostatic and nephrotoxic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 80; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGETLRQWLARAP 15
 |||||
 DB 3 IEGETLRQWLARAP 17

RESULT 12
 ADQ16611
 ID ADQ16611 standard; peptide; 18 AA.
 XX
 AC ADQ16611;
 DT 09-SEP-2004 (first entry)
 DE TPO mimetic peptide with random flanking residues SEQ ID NO:31.
 XX
 DE Immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX
 OS Unidentified.
 OS
 XX NO2004050017-A2.
 PN 17-JUN-2004.
 PD 17-NOV-2003; 2003WO-US036894.
 XX
 PF 17-NOV-2003; 2003WO-US036894.
 XX
 PR 02-DEC-2002; 2002US-00307724.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Frederickson S, Renshaw M;
 XX
 DR WPI, 2004-460973/43.
 DR N-PSDB; ADQ16612.
 XX
 PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX
 PS Example 1; SEQ ID NO 31; 107pp; English.
 XX
 CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 80; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGETLRQWLARAP 15
 |||||
 DB 3 IEGETLRQWLARAP 17

RESULT 13
 ADQ16619
 ID ADQ16619 standard; peptide; 18 AA.
 XX
 AC ADQ16619;
 DT 09-SEP-2004 (first entry)
 DE TPO mimetic peptide with random flanking residues SEQ ID NO:39.
 XX
 DE Immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX
 OS Unidentified.
 OS
 XX NO2004050017-A2.
 PN 17-JUN-2004.
 PD 17-NOV-2003; 2003WO-US036894.
 XX
 PF 17-NOV-2003; 2003WO-US036894.
 XX
 PR 02-DEC-2002; 2002US-00307724.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Frederickson S, Renshaw M;
 XX
 DR WPI, 2004-460973/43.
 DR N-PSDB; ADQ16620.
 XX
 PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX
 PS Example 1; SEQ ID NO 39; 107pp; English.
 XX
 CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 80; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGETLRQWLARAP 15
 |||||
 DB 3 IEGETLRQWLARAP 17

RESULT 14

ADQ16621
ID ADQ16621 standard; peptide; 18 AA.

XX ADQ16621;

DT 09-SEP-2004 (first entry)

XX TPO mimetic peptide with random flanking residues SEQ ID NO:41.

XX immunoglobulin; complementarily determining region; CDR; peptide mimetic;

KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

XX immunotherapy; thrombocytopenia.

OS Unidentified.

XX WO2004050017-A2.

XX 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Frederickson S, Renshaw M,

DR WPI; 2004-460973/43.

DR N-PSDB; ADQ16622.

PT New immunoglobulin molecule comprising a region, where two

PT complementarity determining regions (CDRs) are replaced with EPO mimetic

PT or a TPO mimetic, useful for treating thrombocytopenia.

XX Example 1; SEQ ID NO 41; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

CC comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarity determining regions (CDRs) are replaced

CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

CC invention has immunosuppressive activity, and may have a use in

CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or

CC treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.

CC The present sequence represents a TPO mimetic peptide with flanking

CC residues.

CC Sequence 18 AA;

XX Query Match 100.0%; Score 80; DB 8; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-06;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAAP 15

DB 3 IEPTLRQWLAAAP 17

RESULT 15

ADQ16646
ID ADQ16646 standard; peptide; 18 AA.

XX ADQ16646;

DT 09-SEP-2004 (first entry)

XX TPO mimetic peptide SEQ ID NO:65.

KW immunoglobulin; complementarily determining region; CDR; peptide mimetic;

KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

XX immunotherapy; thrombocytopenia.

OS Unidentified.

XX WO2004050017-A2.

XX 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Frederickson S, Renshaw M;

DR WPI; 2004-460973/43.

DR N-PSDB; ADQ16645.

PT New immunoglobulin molecule comprising a region, where two

PT complementarity determining regions (CDRs) are replaced with EPO mimetic

PT or a TPO mimetic, useful for treating thrombocytopenia.

XX Example 4; SEQ ID NO 66; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

CC comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarity determining regions (CDRs) are replaced

CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

CC invention has immunosuppressive activity, and may have a use in

CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or

CC treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.

CC The present sequence represents a TPO mimetic peptide of the invention.

XX Sequence 18 AA;

XX Query Match 100.0%; Score 80; DB 8; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-06;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAAP 15

DB 3 IEPTLRQWLAAAP 17

Search completed: December 20, 2004, 13:51:00

Job time : 155 secs

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OM protein - protein search, using sw model

Run on: December 20, 2004, 13:45:52 ; Search time 37 Seconds

(Without alignments)
26.886 Million cell updates/sec

Title: US-10-006-593-2

Sequence: 1 IEGBTLRQMLAARAP 15

Scoring table:

BLOSUM62

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCFUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	91.2	14	2 US-08-764-640-13	Sequence 13, Appl
2	73	91.2	14	2 US-08-764-640-193	Sequence 13, Appl
3	73	91.2	14	3 US-08-973-225-13	Sequence 13, Appl
4	73	91.2	14	3 US-08-973-225-193	Sequence 13, Appl
5	73	91.2	14	3 US-08-973-225-193	Sequence 13, Appl
6	73	91.2	14	3 US-08-973-225-193	Sequence 13, Appl
7	73	91.2	14	3 US-08-973-225-193	Sequence 13, Appl
8	73	91.2	14	3 US-08-973-225-193	Sequence 13, Appl
9	73	91.2	14	3 US-08-973-225-193	Sequence 13, Appl
10	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
11	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
12	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
13	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
14	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
15	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
16	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
17	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
18	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
19	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
20	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
21	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
22	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
23	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
24	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
25	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
26	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl
27	73	91.2	14	4 US-08-973-225-193	Sequence 13, Appl

28	73	91.2	15	4 US-09-832-230A-17	Sequence 17, Appl
29	73	91.2	15	4 US-09-832-230A-185	Sequence 18, Appl
30	73	91.2	16	2 US-08-764-640-18	Sequence 18, Appl
31	73	91.2	16	2 US-08-764-640-194	Sequence 18, Appl
32	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
33	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
34	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
35	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
36	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
37	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
38	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
39	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
40	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
41	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
42	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
43	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
44	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl
45	73	91.2	16	2 US-08-764-640-232	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-764-640-13
Sequence 13, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Wirtz, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Depierre, Randolph B.
APPLICANT: Podcutt, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-13

Query Match 91.2%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAAR 14
DB 1 IEPTLRQWLAAAR 14

RESULT 2

US-08-764-640-193
Sequence 193, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Depirnce, Randolph B.
APPLICANT: Poddaturi, Surekha
APPLICANT: Yan, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-193

Query Match 91.2%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAAR 14
DB 1 IEPTLRQWLAAAR 14

RESULT 3
US-08-973-225-13
Sequence 13, Application US/08973225A

Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Duffin, David J.
APPLICANT: Gates, Christian
APPLICANT: Haselden, Sherill S.
APPLICANT: Mattheakis, Larry C.
APPLICANT: Schatz, Peter J.
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-08-973-225-13

Query Match 91.2%; Score 73; DB 3; Length 14;

Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAAR 14

DB 1 IEPTLRQWLAAAR 14

RESULT 4

US-08-973-225-193

Sequence 193, Application US/08973225A

Patent No. 6083913

GENERAL INFORMATION:

APPLICANT: Dower, William J.

APPLICANT: Barrett, Ronald W.

APPLICANT: Cwiria, Steven E.

APPLICANT: Duffin, David J.

APPLICANT: Gates, Christian

APPLICANT: Haselden, Sherill S.

APPLICANT: Mattheakis, Larry C.

APPLICANT: Schatz, Peter J.

APPLICANT: Wagstrom, Christopher R.

APPLICANT: Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-08-973-225-193

Query Match 91.2%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
DB 1 IEGPTLRQWLARA 14

RESULT 5
US-09-244-298A-13
Sequence 13, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirle, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Depinice, Randolph B.
APPLICANT: Poddaturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A

FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
US-09-244-298A-13

Query Match 91.2%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
DB 1 IEGPTLRQWLARA 14

RESULT 6
US-09-244-298A-193
Sequence 193, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirle, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Depinice, Randolph B.
APPLICANT: Poddaturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear

MOLECULE TYPE: peptide
US-09-244-298A-193

Query Match 91.2%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
DB 1 IEGPTLRQWLAAARA 14

RESULT 7
US-09-516-704-13

Sequence 13, Application US/09516704
Patent No. 6251864

GENERAL INFORMATION:

APPLICANT: Dower, William J.

Barrett, Ronald W.

Cwila, Steven E.

Gates, Christian

Schatz, Peter J.

Balaubramanian, Palaniappan

Magstrom, Christopher R.

Hendren, Richard W.

Deprince, Randolph B.

Poduturi, Surekha

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR

NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:

ADDRESS: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704

FILING DATE: 01-Mar-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-516-704-13

Query Match 91.2%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
DB 1 IEGPTLRQWLAAARA 14

RESULT 8
US-09-516-704-193

Sequence 193, Application US/09516704

Patent No. 6251864

GENERAL INFORMATION:

APPLICANT: Dower, William J.

Barrett, Ronald W.

Cwila, Steven E.

Gates, Christian

Schatz, Peter J.

Balaubramanian, Palaniappan

Magstrom, Christopher R.

Hendren, Richard W.

Deprince, Randolph B.

Poduturi, Surekha

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR

NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:

ADDRESS: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704

FILING DATE: 01-Mar-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 193:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 193:

US-09-516-704-193

Query Match 91.2%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
DB 1 IEGPTLRQWLAAARA 14

RESULT 9
US-09-549-090-13

Sequence 13, Application US/09549090

Patent No. 6465430

GENERAL INFORMATION:

APPLICANT: Dower, William J.

Barrett, Ronald W.

Cwila, Steven E.

Duffin, David J.

Gates, Christian

Haseelden, Sherill S.

Mattheakis, Larry C.

Schatz, Peter J.

Magstrom, Christopher R.

Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/549,090

FILING DATE: 13-Apr-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/973,225

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-549-090-13

Query Match 91.2%; Score 73; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLARA 14

Db 1 IEPTLRQWLARA 14

RESULT 10

US-09-549-090-193

Sequence 193, Application US/09549090

Patent No. 6465430

GENERAL INFORMATION:

APPLICANT: Dower, William J.

Barrett, Ronald W.

Cuifia, Steven E.

Duffin, David J.

Gates, Christian

Haseelden, Sherrill S.

Matheakis, Larry C.

Schaltz, Peter J.

Wagstrom, Christopher R.

Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/549,090

FILING DATE: 13-Apr-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/973,225

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 193:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 193:

US-09-549-090-193

Query Match 91.2%; Score 73; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLARA 14

Db 1 IEPTLRQWLARA 14

RESULT 11

US-09-832-230A-13

Sequence 13, Application US/09832230A

Patent No. 6506362

GENERAL INFORMATION:

APPLICANT: Dower, William J. et al

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

RECEPTOR

NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/832,230A

FILING DATE: 10-Apr-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-832-230A-13

Query Match 91.2%; Score 73; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAARA 14
DB 1 IEPTLRQWLAAARA 14

RESULT 12

US-09-832-230A-193
Sequence 193, Application US/09832230A
Patent No. 6506362
GENERAL INFORMATION:
APPLICANT: Dower, William J. et al
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/832,230A
FILING DATE: 10-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 193:

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:

US-09-832-230A-193

Query Match 91.2%; Score 73; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAARA 14
DB 1 IEPTLRQWLAAARA 14

RESULT 13

US-09-428-082B-13
Sequence 13, Application US/09428082B
Patent No. 6660843

GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 13

LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TMP
US-09-428-082B-13

Query Match 91.2%; Score 73; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAARA 14
DB 1 IEPTLRQWLAAARA 14

RESULT 14

US-09-428-082B-26
Sequence 26, Application US/09428082B
Patent No. 6660843

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TPO-MIMETIC PEPTIDE
NAME/KEY: misc_feature
LOCATION: (14)..(14)
OTHER INFORMATION: At position 14, amino acid linker to an identical sequence
US-09-428-082B-26

Query Match 91.2%; Score 73; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAARA 14
DB 1 IEPTLRQWLAAARA 14

RESULT 15

US-09-428-082B-29
Sequence 29, Application US/09428082B
Patent No. 6660843

GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371

PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TPO-MIMETIC PEPTIDE
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(16)
OTHER INFORMATION: Position 16 bromoacetyl group linked to sidechain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(14)
OTHER INFORMATION: At position 14, amino acid linker attached N-to-C to Lys and to a
OTHER INFORMATION: nother linker and an identical sequence
US-09-428-082B-29

Query Match 91.2%; Score 73; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
Db 1 IEGPTLRQWLARA 14

Search completed: December 20, 2004, 13:55:42
Job time : 38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 20, 2004, 13:54:22 ; Search time 144 Seconds
(without alignments)
37.274 Million cell updates/sec

Title: US-10-006-593-2

Perfect score: 80
Sequence: 1 IEQPTLRQWLAARAP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA: *
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	15	US-10-006-593-2	Sequence 2, Appl1
2	80	100.0	15	US-10-307-724-2	Sequence 2, Appl1
3	80	100.0	18	US-10-006-593-31	Sequence 31, Appl1
4	80	100.0	18	US-10-006-593-35	Sequence 35, Appl1
5	80	100.0	18	US-10-006-593-37	Sequence 37, Appl1
6	80	100.0	18	US-10-006-593-39	Sequence 39, Appl1
7	80	100.0	18	US-10-006-593-41	Sequence 41, Appl1
8	80	100.0	18	US-10-006-593-43	Sequence 43, Appl1
9	80	100.0	18	US-10-006-593-45	Sequence 45, Appl1
10	80	100.0	18	US-10-006-593-49	Sequence 49, Appl1
11	80	100.0	18	US-10-006-593-66	Sequence 66, Appl1
12	80	100.0	18	US-10-307-724-31	Sequence 31, Appl1
13	80	100.0	18	US-10-307-724-35	Sequence 35, Appl1

14	80	100.0	18	US-10-307-724-37	Sequence 37, Appl1
15	80	100.0	18	US-10-307-724-39	Sequence 39, Appl1
16	80	100.0	18	US-10-307-724-41	Sequence 41, Appl1
17	80	100.0	18	US-10-307-724-43	Sequence 43, Appl1
18	80	100.0	18	US-10-307-724-45	Sequence 45, Appl1
19	80	100.0	18	US-10-307-724-49	Sequence 49, Appl1
20	80	100.0	18	US-10-307-724-66	Sequence 66, Appl1
21	80	100.0	22	US-10-307-724-130	Sequence 130, Appl1
22	80	100.0	128	US-10-307-724-125	Sequence 125, Appl1
23	80	100.0	249	US-10-307-724-124	Sequence 124, Appl1
24	80	100.0	472	US-10-006-593-67	Sequence 67, Appl1
25	80	100.0	472	US-10-307-724-67	Sequence 67, Appl1
26	73	91.2	14	US-10-006-593-1	Sequence 1, Appl1
27	73	91.2	14	US-10-304-160-31	Sequence 31, Appl1
28	73	91.2	14	US-10-083-768-13	Sequence 13, Appl1
29	73	91.2	14	US-10-083-768-193	Sequence 193, Appl1
30	73	91.2	14	US-10-278-364A-5	Sequence 5, Appl1
31	73	91.2	14	US-10-307-724-1	Sequence 1, Appl1
32	73	91.2	14	US-10-609-217-13	Sequence 13, Appl1
33	73	91.2	14	US-10-609-217-26	Sequence 26, Appl1
34	73	91.2	14	US-10-609-217-29	Sequence 29, Appl1
35	73	91.2	14	US-10-609-217-30	Sequence 30, Appl1
36	73	91.2	14	US-10-609-217-32	Sequence 32, Appl1
37	73	91.2	14	US-10-632-388-13	Sequence 13, Appl1
38	73	91.2	14	US-10-632-388-26	Sequence 26, Appl1
39	73	91.2	14	US-10-632-388-29	Sequence 29, Appl1
40	73	91.2	14	US-10-632-388-30	Sequence 30, Appl1
41	73	91.2	14	US-10-632-388-32	Sequence 32, Appl1
42	73	91.2	14	US-10-651-723-13	Sequence 13, Appl1
43	73	91.2	14	US-10-651-723-26	Sequence 26, Appl1
44	73	91.2	14	US-10-651-723-29	Sequence 29, Appl1
45	73	91.2	14	US-10-651-723-30	Sequence 30, Appl1

ALIGNMENTS

RESULT 1
US-10-006-593-2
; Sequence 2, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; FILE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-2

Query Match 100.0%; Score 80; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IEQPTLRQWLAARAP 15
DB 1 IEQPTLRQWLAARAP 15

RESULT 2

US-10-307-724-2
; Sequence 2, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-2

Query Match

Best Local Similarity 100.0%; Score 80; DB 14; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAARAP 15

Db 1 IEPTLRQWLAARAP 15

RESULT 3

US-10-006-593-31
; Sequence 31, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-31

Query Match

Best Local Similarity 100.0%; Score 80; DB 14; Length 18;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAARAP 15

Db 3 IEPTLRQWLAARAP 17

RESULT 4

US-10-006-593-35
; Sequence 35, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-35

Query Match

Best Local Similarity 100.0%; Score 80; DB 14; Length 18;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAARAP 15

Db 3 IEPTLRQWLAARAP 17

RESULT 5

US-10-006-593-37
; Sequence 37, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-37

Query Match

Best Local Similarity 100.0%; Score 80; DB 14; Length 18;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLROWLAARAP 15
| | | | | | | | | | | | | | | | | | | | | |
Db 3 IEGPTLROWLAARAP 17

RESULT 6
US-10-006-593-39

/ Sequence 39, Application US/10006593
/ Publication No. US20030049683A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdiah, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Renshaw, Mark
/ TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
/ FILE REFERENCE: 1087-2
/ CURRENT APPLICATION NUMBER: US/10/006,593
/ CURRENT FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/251,448
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/288,889
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/294,068
/ PRIOR FILING DATE: 2001-05-29
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 39
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-39

Query Match 100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLROWLAARAP 15
| | | | | | | | | | | | | | | | | | | | | |
Db 3 IEGPTLROWLAARAP 17

RESULT 7
US-10-006-593-41

/ Sequence 41, Application US/10006593
/ Publication No. US20030049683A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdiah, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Renshaw, Mark
/ TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
/ FILE REFERENCE: 1087-2
/ CURRENT APPLICATION NUMBER: US/10/006,593
/ CURRENT FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/251,448
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: US 60/288,889
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/294,068
/ PRIOR FILING DATE: 2001-05-29
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 41
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-41

Query Match 100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLROWLAARAP 15
| | | | | | | | | | | | | | | | | | | | | |
Db 3 IEGPTLROWLAARAP 17

RESULT 8
US-10-006-593-43

/ Sequence 43, Application US/10006593
/ Publication No. US20030049683A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdiah, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Renshaw, Mark
/ TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
/ FILE REFERENCE: 1087-2
/ CURRENT APPLICATION NUMBER: US/10/006,593
/ CURRENT FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/251,448
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/288,889
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/294,068
/ PRIOR FILING DATE: 2001-05-29
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-43

Query Match 100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLROWLAARAP 15
| | | | | | | | | | | | | | | | | | | | | |
Db 3 IEGPTLROWLAARAP 17

RESULT 9
US-10-006-593-45

/ Sequence 45, Application US/10006593
/ Publication No. US20030049683A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdiah, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Renshaw, Mark
/ TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
/ FILE REFERENCE: 1087-2
/ CURRENT APPLICATION NUMBER: US/10/006,593
/ CURRENT FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/251,448
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: US 60/288,889
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/294,068
/ PRIOR FILING DATE: 2001-05-29
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 45
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-45

Query Match 100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IEGPTLRQWLAAAP 15
Db 3 IEGPTLRQWLAAAP 17

RESULT 10
US-10-006-593-49
Sequence 49, Application US/10006593
Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-49

Query Match 100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEGPTLRQWLAAAP 15
Db 3 IEGPTLRQWLAAAP 17

RESULT 11
US-10-006-593-66
Sequence 66, Application US/10006593
Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: TPO mimetic peptide with flanking sequence
US-10-006-593-66

Query Match 100.0%; Score 80; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IEGPTLRQWLAAAP 15
Db 3 IEGPTLRQWLAAAP 17

RESULT 12
US-10-307-724-31
Sequence 31, Application US/10307724
Publication No. US20030232972A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2c1p
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-31

Query Match 100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEGPTLRQWLAAAP 15
Db 3 IEGPTLRQWLAAAP 17

RESULT 13
US-10-307-724-35
Sequence 35, Application US/10307724
Publication No. US20030232972A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2c1d
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn version 3.2
SEQ ID NO 35
LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence

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/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-35

Query Match          100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IEGPTLRQWLAAAP 15
Db      3 IEGPTLRQWLAAAP 17

RESULT 14
US-10-307-724-37
/ Sequence 37; Application US/10307724
/ Publication No. US20030232972A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowditch, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Renshaw, Mark
/ TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
/ FILE REFERENCE: 1087-2c1p
/ CURRENT APPLICATION NUMBER: US/10/307,724
/ CURRENT FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: US 60/251,448
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: US 60/288,889
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/294,068
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: US 10/006,593
/ PRIOR FILING DATE: 2001-12-05
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 37
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-37

Query Match          100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IEGPTLRQWLAAAP 15
Db      3 IEGPTLRQWLAAAP 17

RESULT 15
US-10-307-724-39
/ Sequence 39; Application US/10307724
/ Publication No. US20030232972A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowditch, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Renshaw, Mark
/ TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
/ FILE REFERENCE: 1087-2c1p
/ CURRENT APPLICATION NUMBER: US/10/307,724
/ CURRENT FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: US 60/251,448
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: US 60/288,889
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/294,068
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: US 10/006,593
/ PRIOR FILING DATE: 2001-12-05
/ NUMBER OF SEQ ID NOS: 134
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/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 39
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-39

Query Match          100.0%; Score 80; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IEGPTLRQWLAAAP 15
Db      3 IEGPTLRQWLAAAP 17
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Search completed: December 20, 2004, 14:06:44
Job time : 144 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 20, 2004, 13:45:26 / Search time 38 Seconds

(without alignments)
37.960 Million cell updates/sec

Title: US-10-006-593-2

Perfect score: 80
Sequence: 1 IEGETLRQWLAAAP 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR.79.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.5	61.9	333	2	A36925
2	47	58.8	296	2	AG0147
3	46	57.5	306	2	D70601
4	46	57.5	400	2	C87021
5	44.5	55.6	436	2	JC4742
6	44	55.0	200	2	T23485
7	44	55.0	207	2	T37464
8	44	55.0	536	1	SYCEB
9	44	55.0	536	2	E85558
10	44	55.0	536	2	A99708
11	44	55.0	664	2	H83962
12	44	55.0	762	2	H83415
13	44	53.8	204	2	T44257
14	43	53.8	285	2	G71337
15	43	53.8	664	2	G89894
16	43	53.8	683	2	B71325
17	43	53.8	825	2	JC4163
18	42	52.5	352	2	G83636
19	42	52.5	438	2	G87337
20	42	52.5	473	2	E84851
21	42	52.5	1019	2	T11560
22	42	52.5	2617	2	A82136
23	41	51.2	195	2	F91171
24	41	51.2	195	2	F86017
25	41	51.2	195	2	S47694
26	41	51.2	249	2	E87575
27	41	51.2	306	2	T45453
28	41	51.2	326	2	C24430
29	41	51.2	336	1	DBPZG

30	41	51.2	337	2	A35080	glyceraldehyde-3-p
31	41	51.2	338	1	DE163C	glyceraldehyde-3-p
32	41	51.2	338	2	JQ1287	glyceraldehyde-3-p
33	41	51.2	339	1	B70936	probable serine/th
34	41	51.2	401	2	G87552	conserved hypochet
35	41	51.2	719	2	B95325	conserved hypochet
36	41	51.2	750	2	A97501	topoisomerase IV c
37	41	51.2	750	2	AE2719	topoisomerase IV c
38	40	50.0	229	2	S25204	srnx protein - Str
39	40	50.0	321	2	C70653	probable prephenat
40	40	50.0	463	2	S27491	hypothetical prote
41	40	50.0	518	2	AD2315	hypothetical prote
42	40	50.0	530	2	A81958	probable permease
43	40	50.0	531	2	E81015	ABC transporter, p
44	40	50.0	648	1	H69878	probable protein k
45	40	50.0	656	2	S30484	pol polyprotein -

ALIGNMENTS

RESULT 1

transcription activator LysR-type CbDR - Xanthobacter flavus
C:Species: Xanthobacter flavus
C>Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text_change 09-Jul-2004
C/Accession: A36925; S15578; S35408
R:van den Bergh, E.R.E.; Dijkhuizen, L.; Meijer, W.G.
J. Bacteriol. 175, 6097-6104, 1993
A>Title: CbDR, a LysR-type transcriptional activator, is required for expression of the
A/Reference number: A36925; MUID:94012468; PMID:8407781
A/Accession: A36925
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333 <VAN>
A/Cross-references: UNIPROT:P25545; EMBL:Z22705; NID:9297851; PTDN:CA80406.1; PTD:G581
R:Meijer, W.G.; Arndberg, A.C.; Enquist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen
Mol. Gen. Genet. 225, 320-330, 1991
A>Title: Identification and organization of carbon dioxide fixation genes in Xanthobact
A/Reference number: S15573; MUID:91172133; PMID:1900916
A/Accession: S15578
A/Molecule type: DNA
A/Residues: 1-150 <MEI>
A/Cross-references: EMBL:X17252
C/Genetics:
A:Gene: cdbR
A/Start codon: GTG
C/Superfamily: transcription activator LysR-type
C/Keywords: DNA binding; transcription regulation

Query Match 61.9%; Score 49.5; DB 2; Length 333;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 IEGETLRQWLAAAP 14
Db 264 VEGLPVVRQWLAAVRA 278

RESULT 2
AG0147
probable membrane protein YPO1203 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG0147
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AG0147
A/Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-296 <KUR>
 A:Cross-references: UNIPROT:Q8ZGS7; GB:AL590842; PIDD:CA09042.1; PID:g15979263; GSPDB:C
 C:Genetics:
 A:Gene: YP01203

Query Match 58.8%; Score 47; DB 2; Length 296;
 Best Local Similarity 81.8%; Pred. No. 3.5;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PTLRQMLAAR 14
 |||||
 Db 66 PTLRQMAASA 76

RESULT 3

UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galu [similarity] - Mycobacteri
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: D70601

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 ; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: D70601

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-306 <COL>

A:Cross-references: UNIPROT:O05576; GB:Z94752; GB:AL123456; NID:G3261731; PIDD:CA08153.

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: galu

C:Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase

Query Match 57.5%; Score 46; DB 2; Length 306;
 Best Local Similarity 72.7%; Pred. No. 5.3;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GPTLRQMLAR 13
 |||||
 Db 290 GPDLRRLVAR 300

RESULT 4

serine-threonine protein kinase [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: C87021

R:Coile, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 eam, M.A.; Rutherford, K.M.

R:J. Davies, R.M.; Devlin, K.; Dutroy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 Nature 403, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A>Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: C87021

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 <STO>

A:Cross-references: UNIPROT:O69568; GB:AL450380; NID:g13092968; PIDD:CA031278.1; GSPDB:C

C:Genetics:

A:Gene: ML0897

C:Superfamily: Mycobacterium tuberculosis probable serine/threonine-specific protein kin

Query Match 57.5%; Score 46; DB 2; Length 400;
 Best Local Similarity 66.7%; Pred. No. 7;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 IEQPTLRQMLAARAP 15
 |||||
 Db 86 IEQPTLRQMLAARAP 100

RESULT 5

transposase - Corynebacterium glutamicum

C:Species: Corynebacterium glutamicum

C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: J04742

R:Corrêa, A.; Pisabarro, A.; Castro, J.M.; Martin, J.F.

Gene 170, 91-94, 1996

A>Title: Cloning and characterization of an IS-like element present in the genome of Br

A:Reference number: J04742; MUID:96200862; PMID:8621097

A:Accession: J04742

A:Molecule type: DNA

A:Residues: 1-436 <COR>

A:Cross-references: UNIPROT:Q45293; EMBL:266534

A:Experimental source: ATCC 13869

A>Note: The authors translated the initiation codon TGR for residue 1 as Val

A>Note: The authors translated the codon ATT for residue 125 as Tyr

C:Genetics:

A:Gene: CTG

F:388-415/Domain: DNA binding #status predicted <DNA>

F:405-415/Region: helix-turn-helix

Query Match 55.6%; Score 44.5; DB 2; Length 436;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 IEQPTLRQMLAARAP 15
 |||||
 Db 206 VEGRSADLRRLAARTP 223

RESULT 6
 T23485
 hypothetical protein K08F4.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T23485

R:Hemby, C.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19746

A:Accession: T23485

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-200 <ML>

A:Cross-references: EMBL:Z68879; PIDD:CAA93088.1; GSPDB:GN00022; CESP:K08F4.11

A:Experimental source: clone K08F4

C:Genetics:

A:Gene: CESP:K08F4.11

A:Map position: 4

A:introns: 45/1; 76/1; 111/3

C:Superfamily: glutathione transferase

Query Match 55.0%; Score 44; DB 2; Length 200;
 Best Local Similarity 61.5%; Pred. No. 7.3;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEQPTLRQMLAAR 13
 |||||
 Db 183 IETPKXEWLAAR 195

RESULT 7

T23464

probable glutathione transferase (EC 2.5.1.18) GST3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T37464
R/Twe, W.N.; Eschbach, M.L.; Walter, R.D.; Henkle-Duehnren, K.
Submitted to the EMBL Data Library, June 1997
A/Description: Paratubercular mediate differential gene expression in *C. elegans*.
A/Reference number: 221702
A/Accession: T37464
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-207 <TAM>
A/Cross-references: UNIPROT:O16116; EMBL:AF010241; PDB:1AAB65419.1
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: GST3
C/Superfamily: glutathione transferase
C/Keywords: transferase

Query Match 55.0%; Score 44; DB 2; Length 207;
Best Local Similarity 61.5%; Pred. No. 7.6;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 IEGETLQWLAAR 13
Db 190 IETPKLQWLAAR 202

RESULT 8
SYCEB
2,3-dihydroxybenzoate-[carrier protein] ligase (EC 6.2.1.-) ente - *Escherichia coli* (str N/Alternate names: 2,3-dihydroxybenzoate-AMP ligase [maximer]; dihydroxybenzoic acid-ac C/Species: *Escherichia coli*
C/Date: 31-Dec-1999 #sequence revision 21-Nov-1997 #text_change 09-Jul-2004
R/Accession: H64792; A48308; A33047; I41058; S08076
R/Bacter: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A.; Rose, D.V.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: H64792
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-536 <BLAT>
A/Cross-references: UNIPROT:P10178; GB:AB000165; GB:U00096; NID:G1786808; PDB:1AAC73695.
A/Experimental source: strain K-12, substrain MG1655
R/Strab: J.F.; Elkins, M.F.; Earhart, C.F.
FEMS Microbiol. Lett. 59, 15-19, 1989
A/Title: Nucleotide sequence of the *Escherichia coli* ente gene.
A/Reference number: A48308; MUID:89290355; PMID:2525505
A/Note: in Medicine 89290355 this citation is erroneously given as volume 50 rather than A/Accession: A48308
A/Molecule type: DNA
A/Residues: 1-368; 'ECCRKSTAR', 379-536 <STA>
A/Cross-references: GB:M27450; EMBL:X15058; NID:G41345; PDB:1CMA33158.1; PDB:G41346
R/Liu, J.; Duncan, K.; Walsh, C.T.
J. Bacteriol. 171, 791-798, 1989
A/Title: Nucleotide sequence of a cluster of *Escherichia coli* enterobactin biosynthesis A/Reference number: A91904; MUID:89123155; PMID:2521622
A/Accession: A32047
A/Molecule type: DNA
A/Residues: 393-536 <LIU>
A/Cross-references: GB:M24148; NID:G304949; PDB:1AA16101.1; PDB:G450380
C/Comment: The enzymatic steps in the condensation of L-serine and 2,3-dihydroxybenzoic ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with C/Comment: The formation of 2,3-dihydroxybenzoyl-AMP has been observed. The rapid react carrier protein) to release AMP, has also been observed.
C/Genetics:
A/Gene: ente
A/Map position: 14 min
C/Function:
A/Description: catalyzes the formation of 2,3-dihydroxybenzoyl-[carrier protein], AMP an A/Pathway: enterobactin biosynthesis
A/Note: this is one component of a membrane-bound multienzyme complex that catalyzes the C/Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

C/Keywords: acid-thiol ligase; enterobactin biosynthesis; membrane-associated complex F:69-526/Domain: acetate-CoA ligase homology <ACT>

Query Match 55.0%; Score 44; DB 1; Length 536;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IEGETLQWLAAR 14
Db 521 VDKKQLQWLAAR 534

RESULT 9
E8558
2,3-dihydroxybenzoate-AMP ligase [imported] - *Escherichia coli* (strain O157:H7, substra C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence revision 16-Feb-2001 #text_change 01-Mar-2002
C/Accession: E85558
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe R/Accession: H64792; A48308; A33047; I41058; S08076
R/Bacter: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A.; Rose, D.V.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: H64792
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-536 <STO>
A/Cross-references: GB:AB005174; NID:G12513487; PDB:1AAG54929.1; GSPDB:GN00145; UMGF:20 A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: ente
C/Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 55.0%; Score 44; DB 2; Length 536;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IEGETLQWLAAR 14
Db 521 VDKKQLQWLAAR 534

RESULT 10
A99708
2,3-dihydroxybenzoate-AMP ligase [imported] - *Escherichia coli* (strain O157:H7, substra C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A99708
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: A99708
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-536 <HAY>
A/Cross-references: UNIPROT:Q8XBV3; GB:BA000007; PDB:1BAB34056.1; PDB:G13360091; GSPDB: A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECG0633
C/Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 55.0%; Score 44; DB 2; Length 536;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IEGETLQWLAAR 14
Db 521 VDKKQLQWLAAR 534

RESULT 11

```

H83962
serine/chreonine protein kinase BH2504 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: H83962
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: H83962
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1564 <SNO>
A:Cross-references: UNIPROT:O9KZ0; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06Z
A:Experimental source: Strain C-125
C:Genetics:
A:Gene: BH2504

Query Match          55.0%; Score 44; DB 2; Length 664;
Best Local Similarity 46.7%; Pred. NO. 25;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Cy 1 IEGPLRQWLAAAP 15
:|||||:
Db 90 VEGPLKELIQORP 104

```

```

RESULT 12
H83415
cirs/crane 1somerae PA1846 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83415
R:Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.T.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: H83415
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-762 <STO>
A:Cross-References: UNIPROT:O91P9; GB:AB004610; GB:AB004091; NID:g9947825; PIDN:AA05223
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: cti, PA1846

```

```

Query Match      55.0%   Score 44;   DB 2;   Length 763;
Best Local Similarity 64.3%   Pred. No. 29;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY      2  EGPTRQWLAAP 15
      |||::|||
db      173  EYATLQKWLAAAP 186

```

RESULT 13
T44257
thiamine-phosphate diphosphorylase (EC 2.5.1.3) [imported] - Rhizobium etli plasmid b
C|Species: Rhizobium etli
C|Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C|Accession: T44257
J|Miranda-Rios, J.; Morera, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sob
J. Bacteriol. 179, 6887-6893, 1997
A|Title: Expression of thiamin biosynthetic genes (thiCOGE) and production of symbiotic
A|Reference number: Z22737; MUID:98037482; PMID:9371431
A|Accession: T44257
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-204 <MIR>
A|Cross-references: UNIPROT:O34294; EMBL:AF004408; NID:G2627325; PIDN:AA045975.1; PID:G2
A|Experimental source: strain CE3

C:Genetics: **thiE**
A:Gene: **thiE**
A:Genome: **plasmid b**
C:Superfamily: **thiE** protein; **thiamin-phosphate pyrophosphorylase** homology
C:Keywords: **transrase**

Query Match	53.8%	Score 43	DB 2	Length 204
Best Local Similarity	88.9%	Pred. No. 11		
Matches	8	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

```
QY      7 RQWLARAP 15
        |||||
Db     191 RQWLAATAP 199
```

RESULT 14

G71337

Probable dimethylidenosine transferase (xsga) - syphilis spirochete
Cispecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
CDate: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
CAccession: G71337

R.Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Wilson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettersack, T.; McDaniel, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A|Reference number: A71250; MUID:98332770; PMID:9655876

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-285 <COL>
A:Cross-references: UNIPROT:O8357; GB:AE001213; GB:AE000520; NID:G3322606; PIDN:AAC653
A:Experimental source: strain Nichols
C:Genetics:
C:Gene: TP0337
C:Superfamily: tRNA (adenine-N6-)-methyltransferase

Query Match	53.8%	Score 43;	DB 2;	Length 285;
Best Local Similarity	64.3%;	Pred. NO. 15;		
Matches	9;	Conservative	1;	Mismatches 4;
				Indels 0;
				Gaps 0;

```
QY      1 IEGPTLRQWLAARA 14
         ||| : ||| |
Db      98 IEGDVLQQWHAATA 111
```

RESULT 15
G89894

```

protein kinase [imported] - Staphylococcus aureus (strain N315)
!Species: Staphylococcus aureus
Date: 10-May-2001 #sequence revision 10-May-2001 #text_change 09-Jul-2004

```

R. Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Ogura, A., Matsui-Ui, Y., Kobayashi, N., Sawano, T., Inoue, R., Kaito, C., Sekimizu, K., C., Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H., Hiratsutsu, K.

Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*
 Reference number: A89758; MUID:21311952; PMID:1418146
 Cancer 357, 1225-1240, 2001

A:Accession: G89894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-664 <KIR>
A:Cross-references: UNIPROT:Q93UP8, GB:BA000018, PID:513701020, PIDN:BA042315.1, GSPDB:
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1063

Query Match	53.8%	Score 43;	DB 2;	Length 664;
Best Local Similarity	46.7%	Pred. No. 36;		
Matches	7;	Conservative	4;	Mismatches 4; Indels 0; Gaps 0

```

1 IEGPTLRQWLARAP 15
||||| : : :
QY

```

Db 90 IECPLEBYIESHP 104

Search completed: December 20, 2004, 13:55:00
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 20, 2004, 13:37:31 ; Search time 188 Seconds
(without alignments)
45.908 Million cell updates/sec

Title: US-10-006-593-2
Perfect score: 80
Sequence: 1 IEGLTRQWLARAP 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	62.5	302	2 Q742B3	Q742B3 mycobacteri
2	50	62.5	302	2 AAS03241	AAS03241 mycobacte
3	49.5	61.9	333	1 CBBR_XANFL	P25545 xanthobacte
4	49	61.3	319	2 Q8Y015	Q8Y015 ralsstonia s
5	49	61.3	319	2 Q9RKM5	Q9RKM5 streptomyc
6	49	61.3	375	2 Q7XPP6	Q7XPP6 oryza sativ
7	48.5	60.6	607	2 Q9LBD4	Q9LBD4 polyanthum
8	48	60.0	252	2 Q8XPO9	Q8XPO9 ralsstonia s
9	48	60.0	766	2 Q9WVZ0	Q9WVZ0 pseudomonas
10	48	60.0	941	2 Q8QUU6	Q8QUU6 infectious
11	47	58.8	296	2 Q8ZGS7	Q8ZGS7 yersinia pe
12	47	58.8	296	2 AAS61189	AAS61189 yersinia
13	46	57.5	153	2 Q8OZRO	Q8OZRO mus musculu
14	46	57.5	167	2 Q88R85	Q88R85 pseudomonas
15	46	57.5	252	2 Q8XV68	Q8XV68 ralsstonia s
16	46	57.5	259	2 Q8PFI7	Q8PFI7 xanthomonas
17	46	57.5	306	2 Q7D906	Q7D906 mycobacteri
18	46	57.5	306	2 Q05576	Q05576 mycobacteri
19	46	57.5	306	2 Q7U0M3	Q7U0M3 mycobacteri
20	46	57.5	400	2 Q69568	Q69568 mycobacteri
21	46	57.5	580	2 Q89RH2	Q89RH2 bradyrhizob
22	46	57.5	766	2 Q33466	Q33466 pseudomonas
23	46	57.5	766	2 Q9R9Y9	Q9R9Y9 pseudomonas
24	46	57.5	766	2 Q88K84	Q88K84 pseudomonas
25	46	57.5	1242	1 NPHN_MOUSE	NPHN_MOUSE mus musculu
26	46	57.5	1256	2 Q9JTX1	Q9JTX1 mus musculu
27	45	56.2	87	2 Q8XZK4	Q8XZK4 ralsstonia s
28	45	56.2	245	2 Q66272	Q66272 erythrobact
29	45	56.2	249	2 Q82989	Q82989 erythrobact
30	45	56.2	278	2 Q9XDVO	Q9XDVO erythrobact
31	45	56.2	421	2 Q7W1X1	Q7W1X1 bordetella

32	45	56.2	421	2 Q7WQUB	Q7WQUB bordetella
33	45	56.2	494	2 Q9ESC6	Q9ESC6 mus musculu
34	45	56.2	550	2 Q73YZ0	Q73YZ0 mycobacteri
35	45	56.2	550	2 AAS04130	AAS04130 mycobacte
36	45	56.2	756	2 Q885P2	Q885P2 pseudomonas
37	45	56.2	1049	2 Q9XBP6	Q9XBP6 mycobacteri
38	45	56.2	1234	1 NPHN_RAT	NPHN_RAT rattus norv
39	45	56.2	1252	2 Q9JIX2	Q9JIX2 rattus norv
40	45	56.2	1256	2 Q9ET59	Q9ET59 mus musculu
41	45	56.2	1256	2 Q9Z585	Q9Z585 mus musculu
42	45	56.6	436	2 Q45293	Q45293 corynebacte
43	44	55.0	207	1 Q7S3_CABEL	Q7S3_CABEL caenorhabdi
44	44	55.0	536	1 ENTE_ECO57	ENTE_ECO57 escherichia
45	44	55.0	536	1 ENTE_ECOLI	ENTE_ECOLI escherichia

ALIGNMENTS

RESULT 1					
Q742B3	PRELIMINARY;	PRT;	302 AA.		
AC Q742B3;					
DT 05-JUL-2004 (TREMBlrel. 27, Created)					
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)					
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)					
DE GALTU.					
GN Name=galtu; OrderedLocusNames=MAP0924;					
OS Mycobacterium paratuberculosis.					
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;					
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;					
OX NCBI_TaxID=1770;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=K10;					
RA Li L., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.;					
RL Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AEO17230; AAS03241.1; -					
DR InterPro; IPR005835; NTP_transferase.					
DR Pfam; PF00483; NTP_transferase; 1.					
DR Complete proteome.					
SO SEQUENCE 302 AA; 32149 MW; 4E5D2B1AB572BAE7 CRC64;					
Query Match					
Best Local Similarity	62.5%;	Score 50;	DB 2;	Length 302;	
Matches 9;	Conservative	0;	Mismatches	2;	Indels 0;
Gaps	0;				
DB	3 GPTLRQWLAR 13				
	286 GPTLRQWLAR 296				
RESULT 2					
AAS03241	PRELIMINARY;	PRT;	302 AA.		
AC AAS03241;					
DT 02-MAR-2004 (TREMBlrel. 27, Created)					
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)					
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)					
DE GALTU.					
GN GALTU OR MAP0924.					
OS Mycobacterium paratuberculosis.					
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;					
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.					
OX NCBI_TaxID=1770;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=K10;					
RA Li L., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.;					
RL Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AEO17230; AAS03241.1; -					
DR SEQUENCE 302 AA; 32149 MW; 4E5D2B1AB572BAE7 CRC64;					

Query Match 62.5%; Score 50; DB 2; Length 302;
 Best Local Similarity 81.8%; Pred. No. 5.4;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GPTLRQWLAR 13
 DB 286 GPDRLQWLAR 296

RESULT 3
 CBBR_XANFL STANDARD; PRT; 333 AA.
 ID CBBR_XANFL
 AC P25545;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE HTH-type transcriptional regulator cbbR (Rubisco operon
 transcriptional regulator)
 GN Name=cbbR; Synonyms=cfxO;
 OS Xanthobacter flavus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Xanthobacter.
 OX NCBI_TaxID=281;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H4-14;
 RX MEDLINE=94012468; PubMed=8407781;
 RA van den Bergh E., Dijkhuizen L., Melijer W.G.,
 RT "CbbR, a *lyrB*-type transcriptional activator, is required for
 RT expression of the autotrophic CO₂ fixation enzymes of Xanthobacter
 RT flavus."
 RL J. Bacteriol. 175:6097-6104(1993).
 RN [2]
 RP SEQUENCE OF 1-150 FROM N.A.
 RC STRAIN=H4-14;
 RX MEDLINE=91172133; PubMed=1900916;
 RA Melijer W.G., Arriberg A.C., Enequist H.G., Terpstra P., Lidstrom M.E.,
 RA Dijkhuizen L.;
 RT "Identification and organization of carbon dioxide fixation genes in
 RT Xanthobacter flavus H4-14."
 RL Mol. Gen. Genet. 225:320-330(1991).
 CC -1- FUNCTION: Transcriptional activator for the cbb operon (cbbLSXFP)
 CC for Rubisco and other Calvin cycle genes. Binds specifically to
 CC two binding sites in the cbbR-cbbL intergenic region.
 CC -1- SIMILARITY: Contains 1 HTH *lyrB*-type DNA-binding domain.

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DR EMBL: Z22705; CA80406.1; -;
 DR EMBL: X17252; -; NOT_ANNOTATED_CDS.
 DR PIR: A36925; A36925.
 DR InterPro: IPR000847; HTH *lyrB*.
 DR InterPro: IPR005119; *lyrB* subet.
 DR InterPro: IPR009058; wing_hlx_DNA_bnd.
 DR Pfam: PF00126; HTH_1; 1.
 DR Pfam: PF03466; *lyrB* subetate; 1.
 DR PRINTS: PR00039; HTHLYSR.
 DR PROSITE: PS50931; HTH *lyrB*; 1.
 DR Activator; DNA-binding; Transcription regulation.
 FT DOMAIN 5 HTH *lyrB*-type.
 FT DNA BIND 22 41 H-T motif (By similarity).
 SO SEQUENCE 333 AA; 36003 MW; 9B375B4FBD21E73 CRC64;

Query Match 61.9%; Score 49.5; DB 1; Length 333;
 Best Local Similarity 66.7%; Pred. No. 7.2;
 Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 IEG-PTLRQWLARA 14
 DB 264 VEGLPVQWLAVRA 278

RESULT 4
 ID Q8Y015 PRELIMINARY; PRT; 91 AA.
 AC Q8Y015;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein RSC1059.
 GN Name=RSC04149; Ordered locus names=RSC1059;
 OS Ralstonia solanacearum (pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cartolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigler P., Thebaud P., Whalen M., Winkler P., Levy M.,
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
 RL Nature 415:497-502(2002).
 RL EMBL: AL646062; CAD14761.1; -;
 KM Complete proteome; Hypothetical protein.

SO SEQUENCE 91 AA; 10321 MW; 2B4DFEB37A528AD CRC64;

Query Match 61.3%; Score 49; DB 2; Length 91;
 Best Local Similarity 46.7%; Pred. No. 2.4;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 IEGPTLRQWLARAP 15
 DB 75 LDGPAVQWLAAQTP 89

RESULT 5
 ID Q9RKM5 PRELIMINARY; PRT; 319 AA.
 AC Q9RKM5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative Merf family transcriptional regulator.
 GN Ordered locus names=SC04102; ORFNames=SCD17.06c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajadream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Bartell B.G., Parkhill J.,
 RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147(2002).

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DR EMBL: AL939118; CAB56383.1; -.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000551; HTH_MerR.
DR InterPro: IPR009061; Putative_DNA_bind.
DR Pfam: PF00376; MerR.1.
DR PRINTS: PR00040; HTHMER.
DR SMART: SM00422; HTH_MER.1.
DR PROSITE: PS50937; HTH_MER.2; 1.
DR Complete proteome; DNA-binding.
SQ SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365E CRC64;

Query Match 61.3%; Score 49; DB 2; Length 319;
Best Local Similarity 66.7%; Pred. No. 8.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EGPTRLQWLAR 13
Db 258 DGPRLREWLAR 269

RESULT 6
Q7XPP6 PRELIMINARY; PRT; 375 AA.
AC Q7XPP6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE OSJNB0053K19.27 protein (OSJNB0060B08.2 protein).
GN Name=OSJNB0053K19.27; Synonyms=OSJNB0060B08.2;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL: AL606645; CAE03519.2; -.
DR EMBL: AL606669; CAE04739.1; -.
DR Gramene; Q7XPP6; -.
DR GO: GO:0005515; F:protein binding; IEA.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR002083; MATR.
DR Pfam: PF00651; BTB; 1.
DR Pfam: PF00917; MATR; 1.
DR SMART: SM00225; BTB; 1.
DR SMART: SM00661; MATR; 1.
DR PROSITE: PS50097; BTB; 1.
DR PROSITE: PS50144; MATR; 1.
SQ SEQUENCE 375 AA; 41043 MW; 20FC6E99E4750816 CRC64;

Query Match 61.3%; Score 49; DB 2; Length 375;
Best Local Similarity 60.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IEGPTLRQWLAR 15
Db 138 MERPRLRQWLAR 152
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RESULT 7
Q9LBD4 PRELIMINARY; PRT; 607 AA.
AC Q9LBD4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Polyangium cellulosum (Sorangium cellulosum).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Sorangineae; Polyangiaceae; Polyangium.
OX NCBI_TaxID=56;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=So ces90;
RC MDLINE=20130945; PubMed=10662695;
RA Molnar I., Schupp T., Ono M., Zirkle R.E., Milnamow M.,
RA Nowak-Thompson B., Engel N., Toupet C., Stratzmann A., Cyr D.D.,
RA Gorlach J., Mayo J.M., Hu A., Goff S., Schmid J., Ligon J.M.;
RT "The biosynthetic gene cluster for the microtubule-stabilizing agents
epothilones A and B from Sorangium cellulosum So ces90.";
RL Chem. Biol. 7:97-109(2000).
DR EMBL: AF210843; AAF26904.1; -.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 607 AA; 66326 MW; F113CA299B25048E CRC64;

Query Match 60.6%; Score 48.5; DB 2; Length 607;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 IEGPTLRQWLAR-AP 15
Db 96 VDPGALRWLWLAGAP 111

RESULT 8
Q8XPQ9 PRELIMINARY; PRT; 252 AA.
AC Q8XPQ9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
GN Name=RS02135; OrderedLocustNames=RS1579;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GM11000;
RC MDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Canus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavié M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguler P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -1- SIMILARITY: Contains 1 HTH LuxR-type DNA-binding domain.
DR EMBL: AL646085; CAD18730.1; -.
DR HSPB; P11470; 1FSR.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR009059; b1_resp_reg1tr_C.
DR InterPro: IPR002197; HTH_Pis.
DR InterPro: IPR000792; HTH_LuxR.
DR Pfam: PF00196; Gere; 1.
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DR PRINTS; PRO1590; HTHFIS.
DR PRINTS; PRO0038; HTHLUXR.
DR PRODOM; PRO00307; HTH LUXR; 1.
DR SMART; SMO0421; HTH LUXR; 1.
RW Complete proteome; DNA-binding; Plasmid; Transcription regulation.
SQ SEQUENCE 255 AA; 27666 MW; 483403EB326FC2E CRC64;
Query Match 60.0%; Score 48; DB 2; Length 252;
Best Local Similarity 53.3%; Pred. NO. 9.8;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 IEPTLRQWLAARAP 15
Db 76 IDTPMRRLATRRP 90
RESULT 9
ID Q9WMW20 PRELIMINARY; PRT; 766 AA.
AC Q9WMW20;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cti.
GN Name=cti;
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DOT-TIE;
RX MEDLINE=99412268; PubMed=10482510;
RA Junker F., Ramos J.L.;
RT "Involvement of the cti/trans isomerase Cti in solvent resistance of
RT Pseudomonas putida DOT-TIE";
RL J. Bacteriol. 181:5693-5700(1999).
DR EMBL; AF10738; AAD41252.1; -
DR InterPro; IPR010706; Cti.
DR InterPro; IPR000345; CytC_heme_B8.
DR InterPro; IPR009056; Cytochrome_c.
DR Pfam; PF06934; Cti, 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 766 AA; 87058 MW; 44A0FC6C2C301FE CRC64;
Query Match 60.0%; Score 48; DB 2; Length 766;
Best Local Similarity 71.4%; Pred. NO. 29;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 EGPTRLQWLAARAP 15
Db 177 EYATLRRLAAGAP 190
RESULT 10
ID Q8QUU6 PRELIMINARY; PRT; 941 AA.
AC Q8QUU6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OMF14L.
OS Infectious spleen and kidney necrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae;
OC Unclassified Iridoviridae.
OX NCBI_TaxID=180170;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21874810; PubMed=11878882;
RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
RA Chan S.M.;
RT "Complete genome analysis of the mandarin fish infectious spleen and
RT kidney necrosis iridovirus";

RL Virology 291:126-139(2001).
DR EMBL; AF371960; AAL98838.1; -
SQ SEQUENCE 941 AA; 106703 MW; EB663998C7F6CE83 CRC64;
Query Match 60.0%; Score 48; DB 2; Length 941;
Best Local Similarity 50.0%; Pred. NO. 36;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 IEPTLRQWLAARA 14
Db 581 VQGPFLAQWICSTPA 594
RESULT 11
ID Q8ZGS7 PRELIMINARY; PRT; 296 AA.
AC Q8ZGS7; Q74WE0; Q7CH89;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative membrane protein (putative transmembrane protein).
GN Name=thar4; OrderedLocustNames=YPO934, YPO1203, Y2985;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebatia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brookes K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham D., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skellern J., Stevens K., Whitehead S., Barrrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=2137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Retherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RX Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RT Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ414147; CAC90042.1; -
DR EMBL; AB013900; AAM6536.1; -
DR EMBL; AB017130; AAS61189.1; -
DR PIR; AG0147; AG0147.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000620; DUF6; 2.
DR Pfam; PF00892; DUF6; 2.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 296 AA; 31378 MW; 45947413DCD54CFP CRC64;
Query Match 58.8%; Score 47; DB 2; Length 296;
Best Local Similarity 81.8%; Pred. NO. 17;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PTLROMAARA 14
 |||||
 Db 66 PTLROMAASA 76

RESULT 12

AA661189 PRELIMINARY; PRT; 296 AA.

AC AA661189; 24-MAR-2004 (TREMBlrel. 27, Created)
 DT 24-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 04-MAY-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative membrane protein.
 GN RHAT4 OR YP0934.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 CX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Hong Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017710; AA661189.1;
 SQ SEQUENCE 296 AA; 31378 MW; 45947413DCD54CF6 CRC64;

Query Match 58.8%; Score 47; DB 2; Length 296;
 Best Local Similarity 81.8%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PTLROMAARA 14
 |||||
 Db 66 PTLROMAASA 76

RESULT 13

Q802K0 PRELIMINARY; PRT; 153 AA.

AC Q802K0; 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Similar to RIKEN cDNA 201010K16 gene (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC048547; AAH48547.1; --
 FT NON_TER
 SQ SEQUENCE 153 AA; 17567 MW; 6AD0DEDA735A2C4 CRC64;

Query Match 57.5%; Score 46; DB 2; Length 153;
 Best Local Similarity 61.5%; Pred. No. 13;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GPTLRQWLAADAP 15
 |||||
 Db 33 GPTLRQWLAASPP 45

RESULT 14

Q888B5 PRELIMINARY; PRT; 167 AA.

AC Q888B5; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocustNames=PSPT0115;
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 CX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RA Bell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Kouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
 RA Uitterback T.R., Van Aken S.B., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
 RA Bender C.L., White O., Fraser C.M., Collier A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 Pseudomonas syringae pv. tomato DC3000."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 DR EMBL; AB016859; AA054644.1; --
 DR TIGR; PSP0115; --
 DR InterPro; IPR001220; Lectin_legB
 DR PROSITE; PS00307; LECTIN_LEGOME_BETA; UNKNOWN 1.
 DR KX
 SQ SEQUENCE 167 AA; 17962 MW; 68714921671FB249 CRC64;

Query Match 57.5%; Score 46; DB 2; Length 167;
 Best Local Similarity 90.0%; Pred. No. 14;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LROMAARAP 15
 |||||
 Db 153 LROMAARAP 162

RESULT 15

Q8XY68 PRELIMINARY; PRT; 252 AA.

AC Q8XY68; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
 GN Name=RS03457; OrderedLocustNames=RS01895;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 CX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=2161879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Broctier P., Camus J.C., Catolico L.,
 RA Chaudier M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gauthier C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigauter P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 CC -1- SIMILARITY: Contains 1 HTH luxR-type DNA-binding domain.
 DR EMBL; AL646067; CAD15597.1; --
 DR HSSP; P11470; 1PSE

DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR InterPro; IPR009059; b1 resp. regltr_C.
 DR InterPro; IPR000792; HTH_luxR.

DR Pfam; PF00196; Gex; 1.
DR PRINTS; PR00038; HTHLUXR.
DR PRODOM; PD000307; HTH LUXR; 1.
DR SMART; SM00421; HTH LUXR; 1.
KW Complete proteome; DNA-binding; Transcription regulation.
SQ SEQUENCE 252 AA; 27945 MW; 17FD89DC6803EFBF CRC64;

Query Match 57.5%; Score 46; DB 2; Length 252;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 IEQPTIKQWLAARAP 15
Db 76 IDTPILRWRFATRSP 90

Search completed: December 20, 2004, 13:54:17
Job time : 192 secs